```
 1   TTGTAACAGA AAATTAAAAT ATACTCCACT CAAGGGAATT CTGTACTTTG CCCTTTTGGT  -99
     AAAGTCTCAT TTACATTTCT AAACCTTTCT TAAGAAAATC GAATTCCTT  TGATCTCTCT  -39

-1   TCTGAATTGC AGAAATCAGA TAAAAACTAC TTGGTGAA ATG ACT TCT TGT CAC ATT   18
                                              M   T   S   C   H   I

 7   GCT GAA GAA CAT ATA CAA AAG GTT GCT ATC TTT GGA GGA ACC CAT GGG     66
     A   E   E   H   I   Q   K   V   A   I   F   G   G   T   H   G

23   AAT GAG CTA ACC GGA GTA TTT CTG GTT AAG CAT TGG CTA GAG AAT GGC    114
     N   E   L   T   G   V   F   L   V   K   H   W   L   E   N   G

39   GCT GAG ATT CAG AGA ACA GGG CTG GAG GTA AAA CCA TTT ATT ACT AAC    162
     A   E   I   Q   R   T   G   L   E   V   K   P   F   I   T   N

55   CCC AGA GCA GTG AAG AAG TGT ACC AGA TAT ATT GAC TGT GAC CTG AAT    210
     P   R   A   V   K   K   C   T   R   Y   I   D   C   D   L   N

71   CGC ATT TTT GAC CTT GAA AAT CTT GGC AAA AAA ATG TCA GAA GAT TTG    258
     R   I   F   D   L   E   N   L   G   K   K   M   S   E   D   L

87   CCA TAT GAA GTG AGA AGG GCT CAA GAA ATA AAT CAT TTA TTT GGT CCA    306
     P   Y   E   V   R   R   A   Q   E   I   N   H   L   F   G   P

103  AAA GAC AGT GAA GAT TCC TAT GAC ATT ATT TTT GAC CTT CAC AAC ACC    354
     K   D   S   E   D   S   Y   D   I   I   F   D   L   H   N*  T

119  ACC TCT AAC ATG GGG TGC ACT CTT ATT CTT GAG GAT TCC AGG AAT AAC    402
     T   S   N   M   G   C   T   L   I   L   E   D   S   R   N   N

135  TTT TTA ATT CAG ATG TTT CAT TAC ATT AAG ACT TCT CTG GCT CCA CTA    450
     F   L   I   Q   M   F   H   Y   I   K   T   S   L   A   P   L

151  CCC TGC TAC GTT TAT CTG ATT GAG CAT CCT TCC CTC AAA TAT GCG ACC    498
     P   C   Y   V   Y   L   I   E   H   P   S   L   K   Y   A   T

167  T   R   S   I   A   K   Y   P   V   G   I   E   V   G   P   Q
```

FIG.1A

```
    ACT CGT TCC ATA GCC AAG TAT CCT GTG GGT ATA GAA GTT GGT CCT CAG  546
     P   Q   G   V   L   R   A   D   I   L   D   Q   M   R   K   M
183 CCT CAA GGG GTT CTG AGA GCT GAT ATC TTG GAT CAA ATG AGA AAA ATG  594
     I   K   H   A   L   D   F   I   H   F   N   E   G   K   E
199 ATT AAA CAT GCT CTT GAT TTT ATA CAT CAT TTC AAT GAA GGA AAA GAA  642
     F   P   P   C   A   I   E   V   Y   K   I   I   E   K   V   D
215 TTT CCT CCC TGC GCC ATT GAG GTC TAT AAA ATT ATA GAG AAA GTT GAT  690
     Y   P   R   D   E   N   G   E   I   A   A   I   I   H   P   N
231 TAC CCC CGG GAT GAA AAT GGA GAA ATT GCT ATC ATC CAT CCT AAT      738
     L   Q   D   Q   W   K   P   L   H   P   G   D   P   M   F
247 CTG CAG GAT CAA GAC TGG AAA CCA CTG CCT GGG GAT CCC ATG TTT      786
     L   T   L   D   G   K   T   I   P   G   G   D   C   T   V
263 TTA ACT CTT GAT GGG AAG ACG ATC CCA CTG GGC GGA GAC TGT ACC GTG  834
     Y   P   V   F   V   N   E   A   A   Y   E   K   E   A
279 TAC CCC GTG TTT GTG AAT GAG GCC GCA TAT TAC GAA AAG AAA GAA GCT  882
     F   A   K   T   T   K   L   T   L   N   A   K   S   I   R   C
295 TTT GCA AAG ACA ACT AAA CTA ACG CTC AAT GCA AAA AGT ATT CGC TGC  930
     C   L   H   .
311 TGT TTA CAT TAG AA ATCACTTCCA GCTTACATCT TACACGGTGT CTTACAAATT   984
CTGCTAGTCT GTAAGCTCCT TAAGAGTAGG GTTGTGCCTT ATTCAACTGC ATACATAGCT  1044
CCTAGCACAG TGCCTTATTC GGTAGGCATC TAAGCAAATT TCTTAAATTA ATTAATATAT  1104
CTTTAAAGAT ATCATATTTT ATGTATGTAG CTTATTCAAA GAAGTGTTTC CTATTCTAT   1164
ATAGTTTATT ATACATGATA CTTGGGTAGC TCAACCATTCT CCTTTGTATT            1224
CAGAATATAA AATTGAAATA GATATATATA AGTTAAAAA AAAAAAAAAA AAA           1277
```

FIG.1B

```
                    10v           20v           30v           40v           50v
HLASP     MTSCHIAEEHIQKVAIFGGTHGNELTGVFLVKHWLENGAEIQRTGLEVKPF
          MTSCH:AE:.I:KVAIFGGTHGNELTGVFLVKHWLEN::EIQRTGLEVKPF
BASPCDNA  MTSCHVAEDPIKKVAIFGGTHGNELTGVFLVKHWLENSTEIQRTGLEVKPF
                    10^           20^           30^           40^           50^
                    60v           70v           80v           90v          100v
HLASP      ITNPRAVKKCTRYIDCDLNRIFDLENLGKKMSEDLPYEVRRAQEINHLFGP
           ITNPRAVKKCTRYIDCDLNR:FD ENLGKK.SEDLPYEVRRAQEINHLFGP
BASPCDNA   ITNPRAVKKCTRYIDCDLNRVFDPENLGKKKSEDLPYEVRRAQEINHLFGP
                    60^           70^           80^           90^          100^
                   110v          120v          130v          140v          150v
HLASP     KDSEDSYDIIFDLHN*TTSNMGCTLILEDSRNNFLIQMFHYIKTSLAPLPCY
          KDSEDSYDIIFDLHN*TTSNMGCTLILEDSRN:FLIQMFHYIKTSLAPLPCY
BASPCDNA  KDSEDSYDIIFDLHN*TTSNMGCTLILEDSRNDFLIQMFHYIKTSLAPLPCY
                   110^          120^          130^          140^          150^
                   160v          170v          180v          190v          200v
HLASP     VYLIEHPSLKYATTRSIAKYPVGIEVGPQPQGVLRADILDQMRKMIKHALD
          VYLIEHPSLKYATTRSIAKYPVGIEVGPQPQGVLRADILDQMRKMI:HALD
BASPCDNA  VYLIEHPSLKYATTRSIAKYPVGIEVGPQPQGVLRADILDQMRKMIQHALD
                   160^          170^          180^          190^          200^
                   210v          220v          230v          240v          250v
HLASP     FIHHFNEGKEFPPCAIEVYKIIEKVDYPRDENGEIAAIIHPNLQDQDWKPL
          FIH:FNEGKEFPPCAIEVYKI: KVDYPR:E:GEI:AIIHP:LQDQDWKPL
BASPCDNA  FIHNFNEGKEFPPCAIEVYKIMRKVDYPRNESGEISAIIHPKLQDQDWKPL
                   210^          220^          230^          240^          250^
                   260v          270v          280v          290v          300v
HLASP     HPGDPMFLTLDGKTIPLGGDCTVYPVFVNEAAYYEKKEAFAKTTKLTLNAK
          HP.DP:FLTLDGKTIPLGGD TVYPVFVNEAAYYEKKEAFAKTTKLTLNA:
BASPCDNA  HPEDPVFLTLDGKTIPLGGDQTVYPVFVNEAAYYEKKEAFAKTTKLTLNAN
                   260^          270^          280^          290^          300^
          310v
HLASP     SIRCCLH
          SIR..LH
BASPCDNA  SIRSSLH
          310^
```
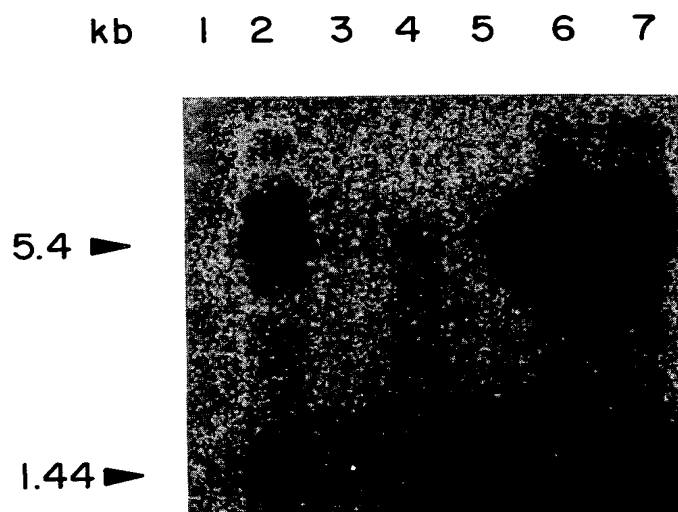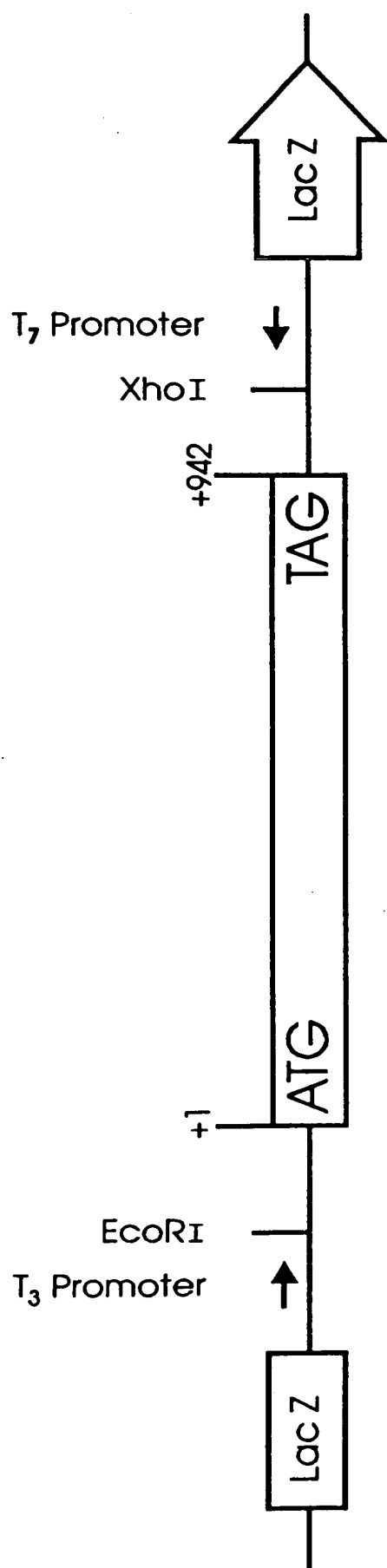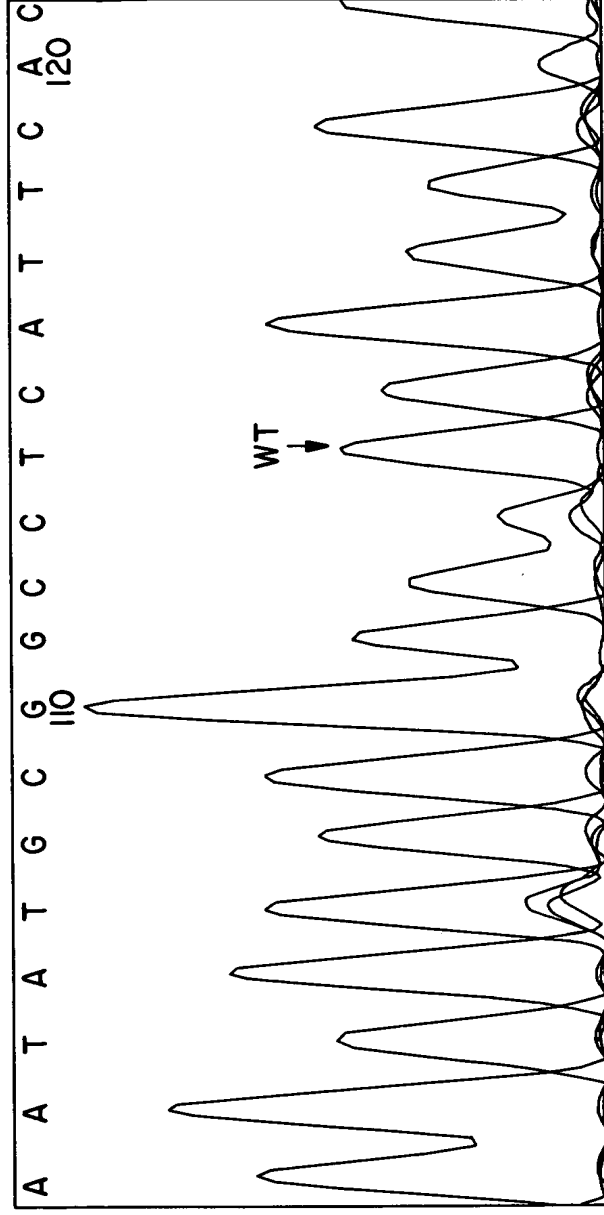
FIG.2

FIG. 3

FIG. 4

FIG.5A

FIG.5B
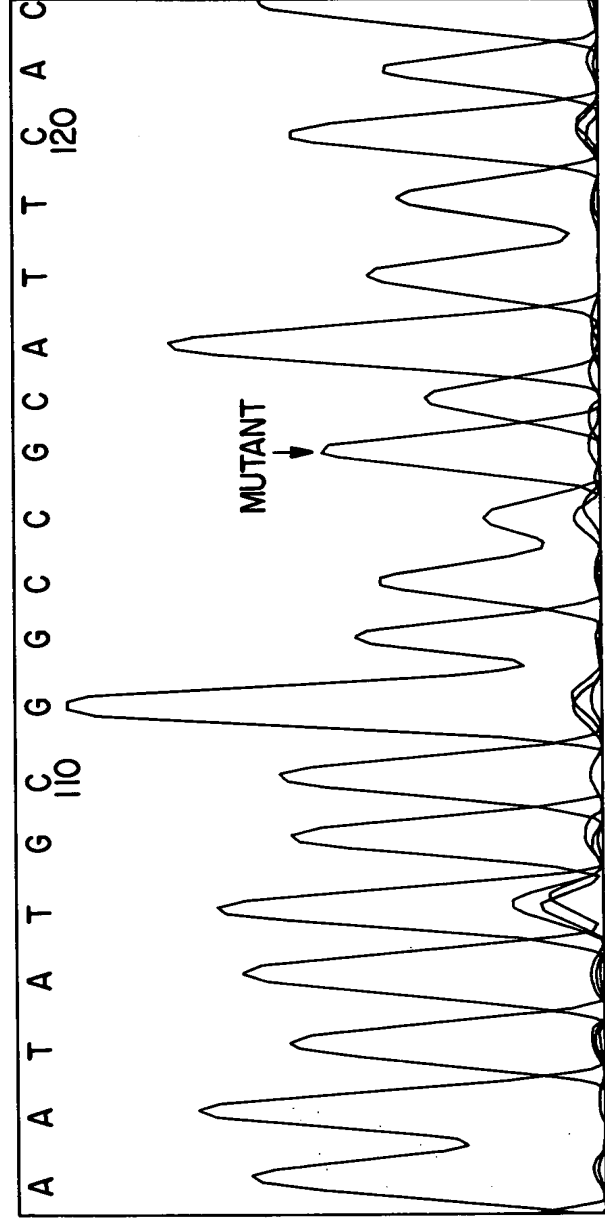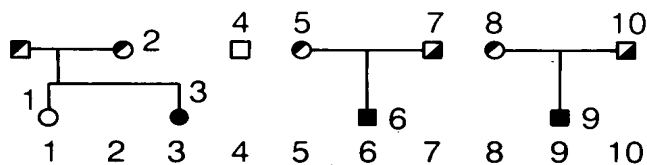
FIG.6A
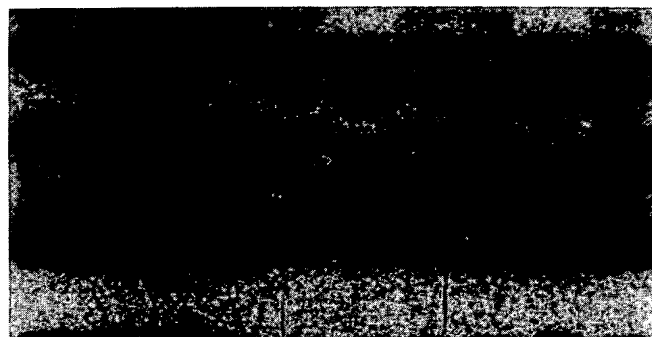
FIG.6B
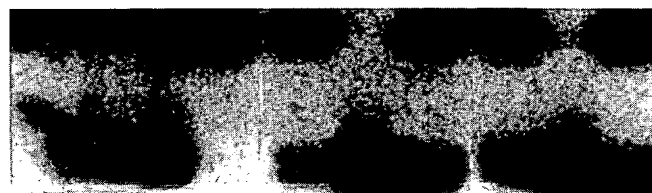
```
      EAM                          M        E    M            N  DSNDSBB
      ASA                          B        C    N            L  STCSESS
      MPE                          O        5    L            A  AYOACAA
      1E3                          2        7    1            4  11111JJ
        /                                                        /////
ATGACTTCTTGTCACATTGCTGAAGAACATATACAAAAGGTTGCTATCTTTGGAGGAACC
----.----+----.----+----.----+----.----+----.----+----.----+   60
TACTGAAGAACAGTGTAACGACTTCTTGTATATGTTTTCCAACGATAGAAACCTCCTTGG

m   t   s   c   h   i   a   e   e   h   i   q   k   v   a   i   f   g   g   t

┃
┗━ START SITE

----.----+----.----+----.----+----.----+----.----+----.----+----.----+


                                        ✓
      N        A    BBH              TSM          RM          H  HHD   TH
      L        L    SCP              RPS          MA          I  HAD   FN
      A        U    AAA              UOE          AE          N  AEE   IF
      3        1    W72              911          11          P  121   11
                      //               ↓/          /             /     /
CATGGGAATGAGCTAACCGGAGTATTTCTGGTTAAGCATTGGCTAGAGAATGGCGCTGAG
----.----+----.----+----.----+----.----+----.----+----.----+   120
GTACCCTTACTCGATTGGCCTCATAAAGACCAATTCGTAACCGATCTCTTACCGCGACTC

h   g   n   e   l   t   g   v   f   l   v   k   h   w   l   e   n   g   a   e


----.----+----.----+----.----+----.----+----.----+----.----+----.----+


      M                            B
      N                            P
      L                            M
      1                            1

ATTCAGAGAACAGGGCTGGAGGTAAAACCATTTATTACTAACCCCAGAGCAGTGAAGAAG
----.----+----.----+----.----+----.----+----.----+----.----+   180
TAAGTCTCTTGTCCCGACCTCCATTTTGGTAAATAATGATTGGGGTCTCGTCACTTCTTC

i   q   r   t   g   l   e   v   k   p   f   i   t   n   p   r   a   v   k   k


----.----+----.----+----.----+----.----+----.----+----.----+----.----+
```

FIG. 7(a)

```
CR     M              M        TH
SS     B              A        FN
PA     O              E        IF
61     2              3        11
                               /
TGTACCAGATATATTGACTGTGACCTGAATCGCATTTTTGACCTTGAAAATCTTGGCAAA
----.----+----.----+----.----+----.----+----.----+----.----+   240
ACATGGTCTATATAACTGACACTGGACTTAGCGTAAAAACTGGAACTTTTAGAACCGTTT

c   t   r   y   i   d   c   d   l   n   r   i   f   d   l   e   n   l   g   k


----.----+----.----+----.----+----.----+----.----+----.----+----.----+


               NM                       BN
               DB                       AS
               EO                       NP
               12                       22
                                        /
AAAATGTCAGAAGATTTGCCATATGAAGTGAGAAGGGCTCAAGAAATAAATCATTTATTT
----.----+----.----+----.----+----.----+----.----+----.----+   300
TTTTACAGTCTTCTAAACGGTATACTTCACTCTTCCCGAGTTCTTTATTTAGTAAATAAA

k   m   s   e   d   l   p   y   e   v   r   r   a   q   e   i   n   h   l   f


----.----+----.----+----.----+----.----+----.----+----.----+----.----+


A              TH        M                                       S
V              FN        B                                       P
A              IF        O                                       O
2              11        2                                       1
               /
GGTCCAAAAGACAGTGAAGATTCCTATGACATTATTTTTGACCTTCACAACACCACCTCT
----.----+----.----+----.----+----.----+----.----+----.----+   360
CCAGGTTTTCTGTCACTTCTAAGGATACTGTAATAAAAACTGGAAGTGTTGTGGTGGAGA

g   p   k   d   s   e   d   s   y   d   i   i   f   d   l   h   n   t   t   s


----.----+----.----+----.----+----.----+----.----+----.----+----.----+


FIG. 7(b)
```

```
   MN A   HBN M           TH E AS              TM
   NL P   GSS N           FN C PC              RS
   LA L   IIP L           IF R YR              UE
   13 1   AH2 1           11 2 11              91
   /       //             /    /                ↓
AACATGGGGTGCACTCTTATTCTTGAGGATTCCAGGAATAACTTTTTAATTCAGATGTTT
----.----+----.----+----.----+----.----+----.----+----.----+   420
TTGTACCCCACGTGAGAATAAGAACTCCTAAGGTCCTTATTGAAAAATTAAGTCTACAAA

 n  m  g  c  t  l  i  l  e  d  s  r  n  n  f  l  i  q  m  f


----.----+----.----+----.----+----.----+----.----+----.----+

        ✓
      TM              N              M  F              E
      RS              L              A  O              C
      UE              A              E  K              O
      91              4              2  1              B
       ↓
CATTACATTAAGACTTCTCTGGCTCCACTACCCTGCTACGTTTATCTGATTGAGCATCCT
----.----+----.----+----.----+----.----+----.----+----.----+   480
GTAATGTAATTCTGAAGAGACCGAGGTGATGGGACGATGCAAATAGACTAACTCGTAGGA

 h  y  i  k  t  s  l  a  p  l  p  c  y  v  y  l  i  e  h  p


----.----+----.----+----.----+----.----+----.----+----.----+

   S           M                                          A
   F           N                                          V
   A           L                                          A
   N           1                                          2
TCCCTCAAATATGCGACCACTCGTTCCATAGCCAAGTATCCTGTGGGTATAGAAGTTGGT
----.----+----.----+----.----+----.----+----.----+----.----+   540
AGGGAGTTTATACGCTGGTGAGCAAGGTATCGGTTCATAGGACACCCATATCTTCAACCA

 s  l  k  y  a  t  t  r  s  i  a  k  y  p  v  g  i  e  v  g


----.----+----.----+----.----+----.----+----.----+----.----+
```

FIG. 7(c)

FIG. 7(d)

```
        S      PBMDD      F              ESASBBSBXBNMDDB
        F      SIBPP      O              CEPCSSFIHALBPPI
        C      TNONN      K              RCYRAAANOMAONNN
        1      11121      1              2111JJN12141211
               ////                      ///  ////////
GCTATCATCCATCCTAATCTGCAGGATCAAGACTGGAAACCACTGCATCCTGGGGATCCC
----.----+----.----+----.----+----.----+----.----+----.----+   780
CGATAGTAGGTAGGATTAGACGTCCTAGTTCTGACCTTTGGTGACGTAGGACCCCTAGGG

 a    i    i    h    p    n    l    q    d    q    d    w    k    p    l    h    p    g    d    p


----.----+----.----+----.----+----.----+----.----+----.----+


                ✓
        N      TM         B              MDBBBDBMA  BBAB     CR      CR
        L      RS         B              BPBSPPIBL  SSCS     SS      SS
        A      UE         V              ONSCUNNOW  ILIM     PA      PA
        3      91         2              121911122  Y112     61      61
               /                         / ////     ///
ATGTTTTTAACTCTTGATGGGAAGACGATCCCACTGGCCGGAGACTGTACCGTGTACCCC
----.----+----.----+----.----+----.----+----.----+----.----+   840
TACAAAAATTGAGAACTACCCTTCTGCTAGGGTGACCCGCCTCTGACATGGCACATGGGG

 m    f    l    t    l    d    g    k    t    i    p    l    g    g    d    c    t    v    y    p


----.----+----.----+----.----+----.----+----.----+----.----+


        SM         HIFA                  H    A
        PN         ATNC                  I    L
        OL         EAUI                  N    U
        11         31H1                  3    1
        /          * //                            *
GTGTTTGTGAATGAGGCCGCATATTACGAAAAGAAAGAAGCTTTTGCAAAGACAACTAAA
----.----+----.----+----.----+----.----+----.----+----.----+   900
CACAAACACTTACTCCGGCGTATAATGCTTTTCTTTCTTCGAAAACGTTTCTGTTGATTT

 v    f    v    n    e    a    a    y    y    e    k    k    e    a    f    a    k    t    t    k

                                                                         a854>c
----.----+----.----+----.----+----.----+----.----+----.----+            E285>A
```

FIG. 7(e)

```
S                      B                HIF   E                                    A
P                      B                NTN   C                                    L
O                      V                FAU   1                                    U
1                      1                31H   5                                    1              ┌─────────┐
                       *                /                                                         │ c914>a  │
CTAACGCTCAATGCAAAAAGTATTCGCTGCTGTTTACATTAGAAATCACTTCCAGCTTAC│ A305>E  │
----.----+----.----+----.----+----.----+----.----+----.----+   └─────────┘ 960
GATTGCGAGTTACGTTTTTCATAAGCGACGACAAATGTAATCTTTAGTGAAGGTCGAATG

l   t   l   n   a   k   s   i   r   c   c   l   h   .   k   s   l   p   a   y


----.----+----.----+----.----+----.----+----.----+----.----+----.----+


                       RM               A     ATM
                       MA               L     FRS
                       AE               U     LUE
                       11               1     291
                       /                      /
ATCTTACACGGTGTCTTACAAATTCTGCTAGTCTGTAAGCTCCTTAAGAGTAGGGTTGTG
----.----+----.----+----.----+----.----+----.----+----.----+   1020
TAGAATGTGCCACAGAATGTTTAAGACGATCAGACATTCGAGGAATTCTCATCCCAACAC

i   l   h   g   v   l   q   i   l   l   v   c   k   l   l   k   s   r   v   v


----.----+----.----+----.----+----.----+----.----+----.----+----.----+


            B   A   RM                       H           D       S
            S   L   MA                       N           D       F
            P   U   AE                       F           E       A
            W   1   11                       3           1       N
                    /
CCTTATTCAACTGCATACATAGCTCCTAGCACAGTGCCTTATTCGGTAGGCATCTAAGCA
----.----+----.----+----.----+----.----+----.----+----.----+   1080
GGAATAAGTTGACGTATGTATCGAGGATCGTGTCACGGAATAAGCCATCCGTAGATTCGT

p   y   s   t   a   y   i   a   p   s   t   v   p   y   s   v   g   i   .   a


----.----+----.----+----.----+----.----+----.----+----.----+----.----+
```

FIG.7(f)

```
           √        √      √             √
        TM      ATM    PATM          TDM         E                        A
        RS      SRS    ASRS          RRS         C                        L
        UE      EUE    CEUE          UAE         R                        U
        91      191    1191          911         V                        1
         /       //    ///                        /
AATTTCTTAAATTAATTAATATATCTTTAAAGATATCATATTTTATGTATGTAGCTTATT
----.----+----.----+----.----+----.----+----.----+----.----+    1140
TTAAAGAATTTAATTAATTATATAGAAATTTCTATAGTATAAAATACATACATCGAATAA

   n  f  l  n  .  l  i  y  l  .  r  y  h  i  l  c  m  .  l  i


----.----+----.----+----.----+----.----+----.----+----.----+



        X                                   N                        A
        M                                   L                        L
        N                                   A                        U
        1                                   3                        1

CAAAGAAGTGTTTCCTATTTCTATATAGTTTATTATACATGATACTTGGGTAGCTCAACA
----.----+----.----+----.----+----.----+----.----+----.----+    1200
GTTTCTTCACAAAGGATAAAGATATATCAAATAATATGTACTATGAACCCATCGAGTTGT

   q  r  s  v  s  y  f  y  i  v  y  y  t  .  y  l  g  s  s  t


----.----+----.----+----.----+----.----+----.----+----.----+



        √                                                             √
        TM                                                            TM
        RS                                                            RS
        UE                                                            UE
        91                                                            91
         /                                                             /
TTCTTAATAAACAGCCTTTGTATTCAGAATATAAAATTGAAATAGATATATATAAAGTTA
----.----+----.----+----.----+----.----+----.----+----.----+    1260
AAGAATTATTTGTCGGAAACATAAGTCTTATATTTTAACTTTATCTATATATATTTCAAT

   f  l  i  n  s  l  c  i  q  n  i  k  l  k  .  i  y  i  k  l


----.----+----.----+----.----+----.----+----.----+----.----+


AAAAAAAAAAAAAAAAAA
----.----+----.--    1277
TTTTTTTTTTTTTTTTTT

   k  k  k  k  k  k


----.----+----.--
```

FIG. 7(g)

```
                        v-21                          v-1
            TCTTCTGAAT TGCAGAAATC AGATAAAAAC TACTTGGTGA


                                        v19
    A ATG ACT TCT TGT CAC ATT GCT GAA GAA CAT ATA CAA
      Met Thr Ser Cys His Ile Ala Glu Glu His Ile Gln
               ^3          ^6          ^9          ^12


         v39                            v59
    AAG GTT GCT ATC TTT GGA GGA ACC CAT GGG AAT GAG
    Lys Val Ala Ile Phe Gly Gly Thr His Gly Asn Glu
             ^15         ^18         ^21         ^24


             v79                            v99
    CTA ACC GGA GTA TTT CTG GTT AAG CAT TGG CTA GAG
    Leu Thr Gly Val Phe Leu Val Lys His Trp Leu Glu
             ^27         ^30         ^33         ^36


             v119                           v139
    AAT GGC GCT GAG ATT CAG AGA ACA GGG CTG GAG GTA
    Asn Gly Ala Glu Ile Gln Arg Thr Gly Leu Glu Val
             ^39         ^42         ^45         ^48


             v159
    AAA CCA TTT ATT ACT AAC CCC AGA GCA GTG AAG AAG
    Lys Pro Phe Ile Thr Asn Pro Arg Ala Val Lys Lys
             ^51         ^54         ^57         ^60


                             v199
    TGT ACC AGA TAT ATT GAC TGT GAC CTG AAT CGC ATT
    Cys Thr Arg Tyr Ile Asp Cys Asp Leu Asn Arg Ile
             ^63         ^66         ^69         ^72


     v219                           v239
    TTT GAC CTT GAA AAC CTT GG  GTAAGACTA TGCTTTGTAT
    Phe Asp Leu Glu Asn Leu Gly
             ^75         ^78


     v259                       v279
    TGTATATGTA TGGATGTTGT GTGAAAGTGG TAGGTGTGT
```

FIG.8

```
                v-42            v-32            v-22            v-12
TATTATCTCA GGCACAGATG TTGTTCATGT TTTTCTTTCT

                v-2                     v8              v18
GCTTATAACA G  C  AAA AAA ATG TCA GAA GAT TTG CCA TAT
                 Lys Lys Met Ser Glu Asp Leu Pro Tyr
              ^80

    v28              v38              v48              v58
GAA GTG AGA AGG GCT CAA GAA ATA AAT CAT TTA TTT
Glu Val Arg Arg Ala Gln Glu Ile Asn His Leu Phe

        v68              v78              v88              v98
GGT CCA AAA GAC AGT GAA GAT TCC TAT GAC ATT ATT
Gly Pro Lys Asp Ser Glu Asp Ser Tyr Asp Ile Ile

            v108             v118             v128
TTT GAC CTT CAC AAC ACC ACC TCT AAC ATG GGG TGC
Phe Asp Leu His Asn Thr Thr Ser Asn Met Gly Cys

        v138             v148             v158             v168
ACT CTT ATT CTT GAG GAT TCC AGG AAT AAC TTT TTA
Thr Leu Ile Leu Glu Asp Ser Arg Asn Asn Phe Leu

            v178             v188             v198
ATT CAG ATG TTT CAT TAC ATT AAG GTAATGTT
Ile Gln Met Phe His Tyr Ile Lys
                                    ^144

        v208          v218          v228
AATGTTATTA ATTTATAAGT CAGCAAAGGA CTTG
```

FIG. 9

```
              v-37           v-27           v-17           v-7
AACATACGGG TTTTTACCCA AGAAAGACGT TTTTGATTTT


              v3             v13            v23
TTTCAG ACT TCT CTG GCT CCA CTA CCC TGC TAC GTT
       Thr Ser Leu Ala Pro Leu Pro Cys Tyr Val
               ^3              ^6              ^9


       v33            v43            v53            v63
TAT CTG ATT GAG CAT CCT TCC CTC AAA TAT GCG ACC
Tyr Leu Ile Glu His Pro Ser Leu Lys Tyr Ala Thr
    ^12            ^15            ^18            ^21


       v73            v83            v93
ACT CGT TCC ATA GCC AAG TAT CCT GTG G   GTAA
Thr Arg Ser Ile Ala Lys Tyr Pro Val
    ^24            ^27            ^30


       v103           v113           v123           v133
GTCATAGTTC CCACTGTCAT AACTCAATAA AATATGTCCT


       v143           v153
AGCTGAAACT CAGAGA
```

FIG.10

```
           v-30            v-20            v-10
TACTTATATA AATGTGACTA TCTCTCCTTC TGTACCTAG   G

            v10             v20             v30
T ATA GAA GTT GGT CCT CAG CCT CAA GGG GTT CTG AGA
  Ile Glu Val Gly Pro Gln Pro Gln Gly Val Leu Arg
  ^177

    v40             v50             v60             v70
GCT GAT ATC TTG GAT CAA ATG AGA AAA ATG ATT AAA
Ala Asp Ile Leu Asp Gln Met Arg Lys Met Ile Lys

        v80             v90             v100
CAT GCT CTT GAT TTT ATA CAT CAT TTC AAT GAA G   GTAAG
His Ala Leu Asp Phe Ile His His Phe Asn Glu
                                            ^211

       v120            v130            v140            v150
TAA TAATGAAGGT AACGTTATCA AACTTAACCA CCAAACATTT

        v160            v170            v180
AAATAACAAT TGGAACCTGG GTCAGA
```

FIG. II

```
                v-38            v-28            v-18            v-8
CCAGAGATGT TTTAGTTGC CATTGATACA TATTGTTTTT

                v2              v12             v22
GTCATAG GA AAA GAA TTT CCT CCC TGC GCC ATT GAG
        Gly Lys Glu Phe Pro Pro Cys Ala Ile Glu
        ^212

        v32             v42             v52             v62
GTC TAT AAA ATT ATA GAG AAA GTT GAT TAC CCC CGG
Val Tyr Lys Ile Ile Glu Lys Val Asp Tyr Pro Arg

        v72             v82             v92
GAT GAA AAT GGA GAA ATT GCT GCT ATC ATC CAT CCT
Asp Glu Asn Gly Glu Ile Ala Ala Ile Ile His Pro

    v102            v112            v122            v132
AAT CTG CAG GTAA CATTTGTTCT TTCTTTAAAA TGTTGAAAAT
Asn Leu Gln
        ^248

        v152            v162            v172            v182
AATAATGCTG TACCTTTGAA TAGAAGTTTA TAGCTCATAC

AGCA
```

<p style="text-align:center">FIG. 12</p>

```
              v-65            v-55            v-45            v-35
GTCTAGAGTC TGACATAAAT TTTTAGAGGA GAAAAACCAA

              v-25            v-15            v-5             v5
ATATAATATA TTTATTTTGA TTGTTTCCTG AGAG GAT CAA GAC
                                         Asp Gln Asp
                                         ^249


          v15             v25             v35
TGG AAA CCA CTG CAT CCT GGG GAT CCC ATG TTT TTA
Trp Lys Pro Leu His Pro Gly Asp Pro Met Phe Leu


v45             v55             v65             v75
ACT CTT GAT GGG AAG ACG ATC CCA CTG GGC GGA GAC
Thr Leu Asp Gly Lys Thr Ile Pro Leu Gly Gly Asp


        v85             v95             v105
TGT ACC GTG TAC CCC GTG TTT GTG AAT GAG GCC GCA
Cys Thr Val Tyr Pro Val Phe Val Asn Glu Ala Ala


            v125            v135            v145
TAT TAC GAA AAG AAA GAA GCT TTT GCA AAG ACA ACT
Tyr Tyr Glu Lys Lys Glu Ala Phe Ala Lys Thr Thr


    v155            v165            v175            v185
AAA CTA ACG CTC AAT GCA AAA AGT ATT CGC TGC TGT
Lys Leu Thr Leu Asn Ala Lys Ser Ile Arg Cys Cys


        v195            v205            v215
TTA CAT TAG AAATCA CTTCCAGCTT ACATCTTACA
Leu His ter
    ^313


v225            v235            v245            v255
CGGTGTCTTA CAAATTCTGC TAGTCTGTAA GCTCCTTAAG


v265
AGTAGGGTT
```

FIG.13